

US-09-768-781-2 (1-1389) x US-09-768-781-4 (1-462)

Qy 1 ATGACACAGACCAACATTCAGAAAGAACCTCGACAAATGGACAGAGTTTATGAAATT 60
Db 1 MetAsnThrArgProGlnHisSerGluArgThrSerThrMetAspArgValTyrGluIle 20
Qy 61 CCTGAGGAGCAAAATGTGGATCCGGTTTCATCTCTGGAGGAGATGTCTATCCGTGGAGCC 120
Db 21 ProGluGluProAsnValAspProValSerSerLeuGluGluAspValIleArgGlyAla 40
Qy 121 AACCCCGGATTTACTTTTCCATTTAGCATCTCTTTTCCACCTTTTGTACTGTGGGAG 180
Db 41 AsnProArgPheThrPheProPheSerIleLeuPheSerThrPheLeuTyrCysGlyGlu 60
Qy 181 GCTGCATCTGTTGTACATGGTTAGAATCTATCGAAAGATAGTGAACCTACTGGATG 240
Db 61 AlaAlaSerAlaLeuTyrMetValArgIleTyrArgLysAsnSerGluThrTyrTrpMet 80
Qy 241 ACATACACCTTTTCTTTCTTATGTTTTCATCCATTTATGTTGGTCCAGTTCACCTCATTTT 300
Db 81 ThrTyrThrPheSerPhePheMetPheSerIleMetValGlnLeuThrLeuIlePhe 100
Qy 301 GTCCACAGAGATCTAGCCAAAGATAAACCGCTATCATTTATGTCATCTAATCTCTTG 360
Db 101 ValHisArgAspLeuAlaLysAspLysProLeuSerLeuPheMetHisLeuLeuLeu 120
Qy 361 GGACCTGTTATCAGATGTTTGAGGCCATGATTAAAGTACCTCACACTGTGGAAGAAAGAG 420
Db 121 GlyProValIleArgCysLeuGluAlaMetIleLysTyrLeuThrLeuTrpLysGlu 140
Qy 421 GAGCAGGAGGAGCCCTATGTCAGCTCACCAGAAAGAGATGCTAATAGATGGCGAGAG 480
Db 141 GluGlnGluProTyrValSerLeuThrArgLysLysMetLeuIleAspGlyGluGlu 160
Qy 481 GTGCTGATAGAAATGGAGGTGGGCACCTCCATCCGAGCCCTGGCTATGCACCGCAATGCC 540
Db 161 ValLeuIleGluTrpGluValGlyHisSerIleArgThrLeuAlaMetHisArgAsnAla 180
Qy 541 TACAAACGTATGTACAGATCAAGCCCTTCTGGGCTCAGTGCCCGACCTGACCTATCAG 600
Db 181 TyrLysArgMetSerGlnIleGlnAlaPheLeuGlySerValProGlnLeuThrTyrGln 200
Qy 601 CTCTATGTGACCTGATCTCTGCAGAGTTCCTCCCTGGGTAGAGTTGTCTAATGGTATT 660
Db 201 LeuTyrValSerLeuIleSerAlaGluValProLeuGlyArgValValLeuMetValPhe 220
Qy 661 TCCCTGGTATCTGTACACCTATGGGCCACCTTTGCAATATGTTGGCTATCCAGATCAAG 720
Db 221 SerLeuValSerValThrTyrGlyAlaThrLeuCysAsnMetLeuAlaIleGlnIleLys 240
Qy 721 TACGATGACTACAAGATTCGCTTGGGCCACTAGAAAGTCTCTGTGCATCACCATCTGGCGG 780
Db 241 TyrAspAspTyrLysIleArgLeuGlyProLeuGluValLeuCysIleThrIleTrpArg 260
Qy 781 ACATTGGAGATCACTTCCCGCTCTGATCTGTGGTCTCTCTCAGCCACTTTGAAATTG 840
Db 261 ThrLeuGluIleThrSerArgLeuLeuIleLeuValLeuPheSerAlaThrLeuLysLeu 280
Qy 841 AAGCTGTGCCCTTCTAGTGTCAACTTCTGTGATCATCTCTTTGAGCCCTGGATTAAAG 900
Db 281 LysAlaValProPheLeuValLeuAsnPheLeuIleIleLeuPheGluProTrpIleLys 300
Qy 901 TTCTGGAGAGTGTGGCCAGATGCCCAATAACATTTGAGAAAACTTCAGCCGGGTCCGC 960
Db 301 PheTrpArgSerGlyAlaGlnMetProAsnAlaIleGluLysAsnPheSerArgValGly 320
Qy 961 ACTCTGGGTGCTGATTTAGTACCAATCTCTATGTCTGATGTCATCACTCTCTTCTGGG 1020
Db 321 ThrLeuValValLeuIleSerValThrIleLeuTyrAlaGlyIleAsnPheSerCysTrp 340
Qy 1021 TCAGCTTGGAGTTGAGCTTGGCAGACAGATCTCTGTCGACAAAGGCGCAGACTGGGA 1080
Db 341 SerAlaLeuGlnLeuArgLeuAlaAspArgAspLeuValAspLysGlyGlnAsnTrpGly 360

Qy 1081 CATATGGCCCTGCACATAGTGTGAGTTGCTAGAGAAATGTGATCATGTCTTGTGTTTT 1140
Db 361 HisMetGlyLeuHisTyrSerValArgLeuValGluAsnValIleMetValLeuValPhe 380
Qy 1141 AAGTCTTTTGGAGTGAAGTGTACTGAATTAATCTGCTCATCTTCCTGATTCCTTGCAGCTC 1200
Db 381 LysPhePheGlyValLysValLeuLeuAsnTyrCysHisSerLeuIleAlaLeuGlnLeu 400
Qy 1201 ATTATGCTTATCTGATTTCCATTGGCTTCATGCTCTTTCTTCCAGTACTTGCATCCA 1260
Db 401 IleIleAlaTyrLeuIleSerIleGlyPheMetLeuLeuPhePheGlnTyrLeuHisPro 420
Qy 1261 TTGGCTCCTACTTCCACCCATAATGCTAGTACACTACCTCCATTGTCTGTCTCACCAG 1320
Db 421 LeuArgSerLeuPheThrHisAsnValValAspTyrLeuHisCysValCysHisGln 440
Qy 1321 CACCTCGGACAGCGTTGAGAACTCAGAGCCACCTTTGAGACTGAAGCAAGGCAAACT 1380
Db 441 HisProArgThrArgValGluAsnSerGluProPheGluThrGluAlaArgGlnSer 460
Qy 1381 GTTGTCT 1386
Db 461 ValVal 462

RESULT 2
US-09-768-781-7
; Sequence 7, Application US/09768781
; Patent No. US20020142376A1
; GENERAL INFORMATION:
; APPLICANT: MERKULOV, Gennady V. et al
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL001057-CIP
; CURRENT APPLICATION NUMBER: US/09768,781
; CURRENT FILING DATE: 2001-01-25
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Mus Musculus
US-09-768-781-7

Alignment Scores:
Pred. No.: 4,94e-220 Length: 449
Score: 2322.00 Matches: 449
Percent Similarity: 100.00% Conservativeness: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 91.31% Indels: 0
DB: 10 Gaps: 0

US-09-768-781-2 (1-1389) x US-09-768-781-7 (1-449)

Qy 40 ATGACAGAGTTTATGAAATTCCTGAGAGCCAAATGTGGATCCGGTTTCATCTCTGGAG 99
Db 1 MetAspArgValTyrGluIleProGluGluProAsnValAspProValSerLeuGlu 20
Qy 100 GAAGATGTCATCCGTGGAGCCAAACCCCGATTACTTTTCCATTAGCATCTTTTCTCC 159
Db 21 GluAspValIleArgLysValAsnProArgPheThrPheProPheSerIleLeuPheSer 40
Qy 160 ACCTTTTGTACTGTGGGAGGCTGCATCTGCTTTGTATGATGTTAGATCTATCGAAAG 219
Db 41 ThrPheLeuTyrCysGlyGluAlaAlaSerAlaLeuTyrMetValArgIleTyrArgLys 60
Qy 220 AATAGTGAACCTTACTGGATGACATACACCTTTTCTTTTATGTTTTCATCCATTATG 279
Db 61 AsnSerGluThrTyrTrpMetThrTyrThrPheSerPhePheMetPheSerSerIleMet 80
Qy 280 GTCCAGTTGACCCCTCATTTTGTCCACAGAGATCTAGCCAAAGATAAACCGCTATCATTA 339

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Db 81 ValGlnLeuThrLeuIlePheValHisArgAspLeuAlaLysAspLysProLeuSerLeu 100
QY 340 TTTATGATCATTAATCCCTTGGGACCTGTTATCAGATGTTTGGAGGCCATGATTAAGTAC 399
DB 101 PheMetHisLeuIleLeuLeuGlyProValIleArgCysLeuGluAlaMetIleLysTyr 120
QY 400 CTCACACTGTGGAAGAAGAGGAGGAGGAGGAGCCCTATGTGACGCTCACCCGAAAGAG 459
DB 121 LeuThrLeuTrpLysGluGlnGluProTyrValSerLeuThrArgLysLys 140
QY 460 ATGCTAATAGATGCGGAGGAGGTCTGATAGAAATGGAGGTGGCCCTCATCCGAGACC 519
DB 141 MetLeuIleAspGlyGluGluValLeuIleGluTrpGluValGlyHisSerIleArgThr 160
QY 520 CTGGCTATGACCGCAATGCTTACAAAGTATGTACAGATCCAGAGCTTCCCTGGGTCA 579
DB 161 LeuAlaMetHisArgAsnAlaTyrLysArgMetSerGlnIleGlnAlaPheLeuGlySer 180
QY 580 GTGCCCGGAGCTGACCTATCAGCTCTATGTAGCGCTGATCTCTGCAGAGGTTCCCTGGGT 639
DB 181 ValProGlnLeuThrTyrGlnLeuTyrValSerLeuIleSerAlaGluValProLeuGly 200
QY 640 AGAGTTGTGCTAATGTTATTTCCCTGATCTGTCTACCTATGGGCGACCCCTTTGCAAT 699
DB 201 ArgValValLeuMetValPheSerLeuValSerValThrTyrGlyAlaThrLeuCysAsn 220
QY 700 ATGTTGGCTATCCAGATCAAGTAGATGACTACAAGATTGCGCTTGGCCCTAGAGATC 759
DB 221 MetLeuAlaIleGlnIleLysTyrAspAspTyrLysIleArgLeuGlyProLeuGluVal 240
QY 760 CTCTGCATCACCATCTCGCGACATGAGATCACTTCCGCGCTCCTGATCTGTGTGCTC 819
DB 241 LeuCysIleThrIleTrpArgThrLeuGluIleThrSerArgLeuLeuIleValLeu 260
QY 820 TTCTCAGCCACTTTGAAATGAAGGCTGTGCGCTTCCCTAGTGTCTCACTTCTCTGATCATC 879
DB 261 PheSerAlaThrLeuLysLeuLysAlaValProPheLeuValLeuAsnPheLeuIle 280
QY 880 CTCTTTGAGCCCTGGATTAAGTTCTGGAGAAGTGGTGGCCGAGATGCCCAATAACATTGAG 939
DB 281 LeuPheGluProTrpIleLysPheTrpArgSerGlyAlaGlnMetProAsnAsnIleGlu 300
QY 940 AAAAACTTCAGCGGGTGGGACCTCTGGTGTCTGATTTCCAGTCACCATCCTCTATGCT 999
DB 301 LysAsnPheSerArgValGlyThrLeuValValLeuIleSerValThrIleLeuTyrAla 320
QY 1000 GGCACTCAACTTCTCTGCTGTGAGCTTTGAGTTGAGGTTGGCAGACAGATCTCGTC 1059
DB 321 GlyLeuAsnPheSerCysTrpSerAlaLeuGlnLeuArgLeuAlaAspArgAspLeuVal 340
QY 1060 GACAAAGGCGAGAACTGGGACATATGGGCTGCATATAGTGTGAGGTGGTATAGAAAT 1119
DB 341 AspLysGlyGlnAsnTrpGlyHisMetGlyLeuHisTyrSerValArgLeuValGluAsn 360
QY 1120 GTGATCATGCTCTGTTGTTTAAAGTTCTTTGGAGTGAAGTTACTGAATTAAGTTCAT 1179
DB 361 ValIleMetValLeuValPheLysPheGlyValLysValLeuLeuAsnTyrCysHis 380
QY 1180 TCCTTGATTCCTTGGAGCTCATTATGCTTATCTGATTTCTCATTTGCTTCTCATCTCCTT 1239
DB 381 SerLeuIleAlaLeuGlnLeuIleIleAlaTyrLeuIleSerIleGlyPheMetLeuLeu 400
QY 1240 TTCTTCAGTACTTGCACTCCGCTCACTTCTTCCACCCATAATGTAGTAGACTACCTC 1299
DB 401 PhePheGlnTyrLeuHisProLeuArgSerLeuPheThrHisAsnValValAspTyrLeu 420
QY 1300 CATTTGTCTGCTGTGACGACCCCTCGGACGAGGTTGAGAACTCAGAGCCACCCCTTT 1359
DB 421 HisCysValCysCysHisGlnHisProArgThrArgValGluAsnSerGluProPhe 440
QY 1360 GACACTGAAGCAAGCAAGTGTGTC 1386
DB 441 GluThrGluAlaArgGlnSerValVal 449
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RESULT 3

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US-09-768-781-3
; Sequence 3, Application US/09768781
; Patent No. US20020142376A1
; GENERAL INFORMATION:
; APPLICANT: MERKULOV, Gennady V. et al
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL001057-CIP
; CURRENT APPLICATION NUMBER: US/09/768,781
; CURRENT FILING DATE: 2001-01-25
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Human
US-09-768-781-3

Alignment Scores:
Pred. No.: 5,78e-218 Length: 449
Score: 2301.00 Matches: 447
Percent Similarity: 99.55% Conservative: 0
Best Local Similarity: 99.55% Mismatches: 2
Query Match: 90.48% Indels: 0
DB: 10 Gaps: 0

US-09-768-781-2 (1-1389) x US-09-768-781-3 (1-449)
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QY 40 ATGACACAGATTTATGAATTCCTGAGAGCCAAATGTGGATCCGGTTTCATCTCTGGAG 99
DB 1 MetAspArgValTyrGluIleProGluInProAsnValAspProValSerSerLeuGlu 20
QY 100 GAACATGTCATCCCTGGAGCCAAACCCCGATTACTTTTCCATTTTAGCATCCTTTTCTCC 159
DB 21 GluAspValIleArgGlyAlaAsnProArgPheThrPheProPheSerIleLeuPheSer 40
QY 160 ACCTTTTGTACTGTGGGAGGCTGCATCTGCTTTGTACATGTTAGATCTATCGAAG 219
DB 41 ThrPheLeuTyrCysGlyGluAlaAlaSerAlaLeuTyrMetValArgIleTyrArgLys 60
QY 220 AATAGTGAACACTTACTCGATGACATACACCTTTTCTTTTCTTTTATGTTTTCATCATG 279
DB 61 AsnSerGluThrTyrArgMetThrTyrThrPheSerPhePheMetPheSerIleMet 80
QY 280 GTCCAGTTGACCCCTCATTTTGTCCACAGAGATCTAGCCAAAGATAAACCGCTATCATTA 339
DB 81 ValGlnLeuThrLeuIlePheValHisArgAspLeuAlaLysAspLysProLeuSerLeu 100
QY 340 TTTATGATCATTAATCCCTTGGGACCTGTTATCAGATGTTTGGAGGCCATGATTAAGTAC 399
DB 101 PheMetHisLeuIleLeuLeuGlyProValIleArgCysLeuGluAlaMetIleLysTyr 120
QY 400 CTCACACTGTGGAAGAAGAGGAGGAGGAGGAGCCCTATGTACGCTCACCCGAAAGAG 459
DB 121 LeuThrLeuTrpLysGluGlnGluProTyrValSerLeuThrArgLysLys 140
QY 460 ATGCTAATAGATGCGGAGGAGGTCTGATAGAAATGGAGGTGGCCCTCATCCGAGACC 519
DB 141 MetLeuIleAspGlyGluGluValLeuIleGluTrpGluValGlyHisSerIleArgThr 160
QY 520 CTGGCTATGACCGCAATGCTTACAAAGTATGTACAGATCCAGAGCTTCCCTGGGTCA 579
DB 161 LeuAlaMetHisArgAsnAlaTyrLysArgMetSerGlnIleGlnAlaPheLeuGlySer 180
QY 580 GTGCCCGGAGCTGACCTATCAGCTCTATGTAGCGCTGATCTCTGCAGAGGTTCCCTGGGT 639
DB 181 ValProGlnLeuThrTyrGlnLeuTyrValSerLeuIleSerAlaGluValProLeuGly 200
QY 640 AGAGTTGTGCTAATGTTATTTCCCTGATCTCTGACCTATGGGCGCACCCCTTTGCAAT 699
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Db 201 ArgValValLeuMetValPheSerLeuValSerValThrTyrGlyAlaThrLeuCysAsn 220
Qy 700 ATGTGGCTATCCAGATCAAGTACGATGACTACAGATTCGGCTTGGCCACTAGAGTC 759
Db 221 MetLeuAlaIleGlnIleLysTyrAspAspTyrLysIleArgLeuGlyProLeuGluVal 240
Qy 760 CTCTGCATCACCATCTGGCGGACATTTGGAGATCAGTTCCTCCGCTCTCTGATTCGTGCTC 819
Db 241 LeuCysIleThrIleTyrArgThrLeuGluIleThrSerArgLeuLeuIleValLeu 260
Qy 820 TTCTCAGCAGCTTTGAAATTAAGGCTGTGCGCTTCTCTAGTGTCTCAACTCTCTGATCATC 879
Db 261 PheSerAlaThrLeuLysLeuLysAlaValProPheLeuValLeuAsnPheLeuIleIle 280
Qy 880 CTCTTGAGCCCTGGATTAAGTTCTGGAGAGTGGTGGCCAGATGCCCAATACATTCAG 939
Db 281 LeuPheGluProTyrPheLysPheTyrArgSerGlyAlaGlnMetProAsnAsnIleGlu 300
Qy 940 AAAAATTTCAGCCGGTGGCACTCTGGTGGTCTCTGATTTTCAGTCCACCATCTCTATGCT 999
Db 301 LysAsnPheSerArgValGlyThrLeuValValLeuIleSerValThrIleLeuTyrAla 320
Qy 1000 GGCATCACTTCTCTGTGTCGTCAGCTTTGAGTGTGAGTGGCGAGACAGATCTCGTC 1059
Db 321 GlyIleAsnPheSerCysTyrPheSerAlaLeuGlnLeuArgLeuAlaAspArgAspLeuVal 340
Qy 1060 GACAAAGGCGAGAACTGGGGACATATGGCGCTGCATAGTGTGAGTGGTGTGAGAT 1119
Db 341 AspLysGlyGlnAsnTyrPheLysMetGlyLeuHisTyrSerValArgLeuValGluAsn 360
Qy 1120 GTGATCATGTCTTGGTCTTAAAGTTCTTGGAGTGAAGTGTACTGAAATTAAGTGTAT 1179
Db 361 ValIleMetValLeuValPheLysPhePheGlyValLysValLeuLeuAsnTyrCysHis 380
Qy 1180 TCCTTGATGTCTTCAGCTCATTAATGCTTATCTGATTTCCATTTGCTGCTTATCTCTT 1239
Db 381 SerLeuIleAlaLeuGlnLeuIleAlaTyrLeuIleSerIleAspPheMetLeuLeu 400
Qy 1240 TTCCTCCAGTACTTCATCCATTCGGCTCACTTTCACCCATTAATGATAGTACACTACCTC 1299
Db 401 PhePheGlnTyrLeuHisProLeuArgSerLeuPheThrHisAsnValValAspTyrLeu 420
Qy 1300 CATTTGTCTGTCTGCACAGCACCCTCGAGCAGGTTGAGAACTTCAGAGCCACCCTTT 1359
Db 421 HisCysValCysCysHisGlnHisProArgThrArgValGluAsnSerGluProPhe 440
Qy 1360 GAGACTGAAGCAAGCAAGTGTCTC 1386
Db 441 GluThrGluAlaArgGlnSerValVal 449

RESULT 4
US-09-768-781-6
; Sequence 6, Application US/09768781
; Patent No. US20020142376A1
; GENERAL INFORMATION:
; APPLICANT: MERKULOV, Gennady V. et al
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL001057-CIP
; CURRENT APPLICATION NUMBER: US/09/768, 781
; CURRENT FILING DATE: 2001-01-25
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 405
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-768-781-6
Alignment Scores: 2.63e-85 Length: 405
Pred. No.: 953.50 Match: 181
Score:
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Percent Similarity: 64.72% Conservative: 85
Best Local Similarity: 44.04% Mismatches: 134
Query Match: 37.50% Indels: 11
DB: 10 Gaps: 4

US-09-768-781-2 (1-1389) x US-09-768-781-6 (1-405)
Qy 136 TTTCCATTAGCATCTTTCTCCACCTTTTGTACTGTGGGAGGCTCATCTGCTTTG 195
Db 1 PheProAlaSerValIleAlaSerValPheLeuPheValAlaGluThrAlaAlaLeu 20
Qy 196 TACATGGTTAGAAATATCGAAAGAATAGTAAACTTACTGGATGACATACACCTTTCT 255
Db 21 TyrLeuSerSerThrTyrArgSerAlaGlyAspArgMetTyrGlnValLeuThrLeuLeu 40
Qy 256 TTCCTTATGTTTTCATCCATTTATGTCAGTTCAGCTCATCTCTTTTGTCCACAGATCTA 315
Db 41 PheSerLeuMetProCysAlaLeuValGlnPheThrLeuLeuPheValHisArgAspLeu 60
Qy 316 GCRAAGATAAACCGCTATCATTTATTTATGATCTTAATCTCTTGGGACCTGTATCAGA 375
Db 61 SerArgAspArgProLeuAlaLeuLeuMetHisLeuLeuGlnLeuGlyProLeuTyrArg 80
Qy 376 TGTTTGGAGGCCATGATTAAGTACCTCACACTGTGGAAGAAAGAGGAGGAGGAGCCCC 435
Db 81 CysCysGluValPheCysIleTyrCys-----GlnSerAspGlnAsnGluPro 97
Qy 436 TATGTACGCTCACCCGAAAGAAAG--ATGCTAATAGATGGCGAGGAGGTGCTGATAGAA 492
Db 98 TyrValSerIleThrLysLysArgGlnMetProLysAspGlyLeuSerGluGluValGlu 117
Qy 493 TGGGAGGTGGCCACTCCATCCGACCCCTGGCTATGCACCGCAATGCCCTACAAACCTATG 552
Db 118 LysGluValGlyGlnAlaGluGlyLysLeuIleThrHisArgSerAlaPheSerArgAla 137
Qy 553 TCACAGATCCAGACCTTCTCTGGCTCAGTCCCGACCTGACCTATCAGCTCTGATGTGAGC 612
Db 138 SerValIleGlnAlaPheLeuGlySerAlaProGlnLeuThrLeuGlnLeuTyrIleThr 157
Qy 613 CTGATCTCTGCAGAGTTCCCTGGGTAGAGTTGTCTAATGGTATTTTCCCTGGTATCT 672
Db 158 ValLeuGluGlnAsnIleThrThrGlyArgCysPheIleMetThrLeuSerLeuLeuSer 177
Qy 673 CTCACCTATGGGGCCACCTTTTGCATATGTTGGTATCCAGATCAAGTACGATGACTAC 732
Db 178 IleValTyrGlyAlaLeuArgCysAsnIleLeuAlaIleLysIleLysTyrAspGluTyr 197
Qy 733 AAGATTCCCTTGGGCCACTAGAGTCTCTCTGCATCACCCTCTGGCGGACATCTGGAGATC 792
Db 198 GluValLysValLysProLeuAlaTyrValCysIlePheLeuTyrArgSerPheGluIle 217
Qy 793 ACTTCCCGCTCTGATCTGCTGCTCTCTCAGCCACTTTGAAATTTGAAGGCTGTGCC 852
Db 218 AlaThrArgValIleValLeuValLeuPheThrSerValLeuLysIleTyrValAla 237
Qy 853 TTCCTAGTCTCAACTTCTCTGATCATCTCTTTGAGCCCTGATTAAGTTCTTGGAGAAGT 912
Db 238 ValIleLeuValAsnPhePheSerPheLeuTyrProTyrIleValPheTyrCysSer 257
Qy 913 GGTGCCAGATGCCCAATAACATTTCAGAAAAAACTTCAGCCGGTTCGGCACTCTGGTGGTC 972
Db 258 GlySerProPheProGluAsnIleGluLysAlaLeuSerArgValGlyThrThrIleVal 277
Qy 973 CTGATTTTCAGTCAACATCTCTATCTGTCGATCAACTTCTCTTGTGGTGTGAGTTCGAG 1032
Db 278 LeuCysPheLeuThrLeuLeuTyrAlaGlyIleAsnMetPheCysTyrPheSerAlaValGln 297
Qy 1033 TTGAGTTGGCAGACAGATCTCTCGACAAAGGCGAAGTGGGACATATATGGCCCTG 1092
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; CURRENT APPLICATION NUMBER: US 09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/006666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006677
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006684
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006699
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006655
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonax Sequence Listing Engine
; SEQ ID NO 37894
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC007064.22
; OTHER INFORMATION: EXPRESSED IN HEART, S
; OTHER INFORMATION: EXPRESSED IN BRAIN, S
; OTHER INFORMATION: EST HUMAN HIT: AA25600
; OTHER INFORMATION: SWISSPROT HIT: P51811
; US-09-864-761-37894

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Alignment Scores:		
Pred. No.:	3,878-27	128
Score:	361.00	66
Percent Similarity:	81.6%	23
Best Local Similarity:	60.5%	20
Query Match:	14.2%	0
DB:	10	0
		Gaps: 0
		Indels: 0
		Mismatches: 20
		Conservative: 23
		Matches: 66
		Length: 128

US-09-768-781-2 (1-1389) x US-09-864-761-37894 (1-128)

Qy	943	AAC	TTCAGCGGGTGGCACTCGTGGTGCTCGATTT	CAGTCACCATCCTCTATGCTGC	1002
			:::		
Db	2	AsnSerAsnMetValGlyThrValLeuMetLeuPheLeuIleThrLeuLeuTyraAla			21
			:::		
Qy	1003	ATCAACTCTCTTGTGTCGTCAGCTTTGCAAGTTGGAGGTGGCAGACAGAGATCTCGTCGAC			1062
			:::		
Db	22	IleAsnPheSerCysTrpSerAlaValIysLeuGlnLeuSerAspAspLysIleAasp			41
			:::		
Qy	1063	AAAGGCCAGAACTGGGGCATATAGCCCTGCACTATAGTGTGAGGTGGTAGAGAANTGTG			1122
			:::		
Db	42	GlyArgGlnArgTrpGlyHisArgIleLeuHisItyrSerPheGlnPheLeuGlusAsnVal			61
			:::		

Qy	1123	ATCATGCTCTGGTTTAAAGTCTTTCGAGTGAAGTGTACTGAATTAATGTCATTC	118
Db	62	IleMetIleLeuValPheArgPheGlyGlyLysThrLeuLeuAsnCysCysAppSer	81
Qy	1183	TTCAATGCTTCGAGCTCAATTAATTCCTTATCTGATTTCCATTTGGCTTCATGCTCCTTTTC	1242
Db	82	LeuIleAlaValGlnLeuIleSerTyLeuLeuAlaThrGlyPheMetLeuLeuPhe	101
Qy	1243	TTCCAGTACTTCATCCATTCGCTCA	1269
Db	102	TyrGlnTyLeuTyProTyrGlnSer	110

RESULT 9

US-09-864-761-35764

; Sequence 35764, Application US/09864761

; Patent No. US20020048763A1

; GENERAL INFORMATION:

; APPLICANT: Penn, Sharron G.

; APPLICANT: Rank, David R.

; APPLICANT: Hanzel, David K.

; APPLICANT: Chen, Wensheng

; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES

; FILE REFERENCE: Aeonica-X-1

; CURRENT APPLICATION NUMBER: US/09/864,761

; CURRENT FILING DATE: 2001-05-23

; PRIOR APPLICATION NUMBER: US 60/180,312

; PRIOR FILING DATE: 2000-02-04

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: US 09/632,366

; PRIOR FILING DATE: 2000-08-03

; PRIOR APPLICATION NUMBER: GB 24263.6

; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00668

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00663

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00662

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00661

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00670

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: US 60/234,687

; PRIOR FILING DATE: 2000-09-21

; PRIOR APPLICATION NUMBER: US 09/608,408

; PRIOR FILING DATE: 2000-06-30

; PRIOR APPLICATION NUMBER: US 09/774,203

; PRIOR FILING DATE: 2001-01-29

; NUMBER OF SEQ ID NOS: 49117

; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1

; SEQ ID NO 35764

; LENGTH: 86

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: MAP TO AL121577.1

; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.2

; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.3

OTHER INFORMATION: MAP TO ALL21577.1
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.3


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; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.4
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.2
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 3.3
; OTHER INFORMATION: EST HUMAN HIT: A1697050.1, EVALUAE 6.00e-43
; OTHER INFORMATION: SWISSPROT HIT: P51813, EVALUAE 1.00e-43
US-09-864-761-35764

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Alignment Scores:	
Pred. No.:	7,91e-09
Score:	174.50
Percent Similarity:	69.86%
Best Local Similarity:	53.42%
Query Match:	6.86%
DB:	10
Gaps:	1
Indels:	1
Mismatches:	21
Conservative:	12
Matches:	39
Length:	86

US-09-768-781-2 (1-1389) x US-09-864-761-35764 (1-86)

QY	427	GAGGAGCCCTATGTCAACCTTACCACCGAAGAAG---ATGCTATATAGATGCCGAGGAGGTG	483
Db	14	GluluProfyrrValSerIleThrLysLeuGlnMetProlysaAsnGlyLeuSerGlu	33
QY	484	CTGATAGAATGGGAGTGGGCCACTCCTCCGAGACCCTGGCTATGCACCGCATGCCTAC	543
Db	34	GlufIeGluLybGluVaIGlyGlnAlaGluGlyLeuIleThriArgSerAlaPhe	53
QY	544	AAACGTGTGCACAGATCCAAGCCTTCCTGGGTTCAGTGCCTGCAGCTGACCTATCAGCTC	603
Db	54	SerArgAlaSerVallieGlnAlaPheLeuGlySerAlaProGlnLeuThrLeuGlnLeu	73
QY	604	TATGTGAGCCTGATCTCTCGACAGAGTTTCCCCTGGGTAGA	642
Db	74	TyrIleSerValMetGlnGlnAspValThrVaIdcIyArq	86

RESULT 10

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US-10-174-590-524
; Sequence 524, Application US/10174590
; Publication No. US20030008352A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C42
; CURRENT APPLICATION NUMBER: US/10/174,590
; CURRENT FILING DATE: 2002-06-18
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 524
; LENGTH: 686
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-174-590-524

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Alignment Scores:	
Pred. No.:	0.000748
Score:	127.00
Percent Similarity:	35.94%
Best Local Similarity:	21.09%
Query Match:	4.99%
Length:	886
Matches:	81
Conservative:	57
Mismatches:	158
Indels:	88

DB:		9	Gaps:	15
	US-09-768-781-2 (1-1389) x US-10-174-590-524 (1-686)			
Qy	157 TCACCTTTTGTACTGTCGGGAGGCTGCATCTGTTTGATCATGTTTAGAATCTATCGA	216 : : :		
Db	9 SerAlaLeuLeuGlnalalaGlInSerAlaArgLeuTyThrValaLysTrPhe	28 : : :		
Qy	217 AAGAATAAGTGAACAATTACTTGGATGACATACACCCTTTCTCTTATATGTTTTCCATC	276 : : : :		
Db	29 ThrThrGlyArgLeuLeuTrpGlyTrpLeualaLeuaLaValLeuProGlyPheLeu	48 : : : :		
Qy	277 ATGGTCGAGTTGACCCCTCAATTTTTCACAGAGATCTAGCCAAGATPAACCGCTATCA	336 : : : : :		
Db	49 ValGlnAlaLeuSerTyrrPheArgAlaAspGlyHisProGlyHisCysSerLeu	68 : : : : :		
Qy	337 TTATTTATGCATCTAACTCTTTGGACCTGTTATCACATGTTTGGAGGCCATGTAAG	396 : : : : :		
Db	69 ValMetLeuHsiLeuLeuGlnLeuGlyValTrpIysArgHisTrpaspAlaLeuThr	88 : : : : :		
Qy	397 TACCTCACATGTGGAAGAACAGGAGGAGGAGGCCTATGTGAGCCTCACC CGAAG	456 : : : : :		
Db	89 SerLeu-----GlnIysGluLeuGlaProHisArgGly-	100 : : : :		
Qy	457 AAGATGCTAATAGATGGCAGGAGTGTGATAGAAATGGAGGTGGGCCCATCCCATCGG	516 : : :		
Db	101 -----Tp-	101 : : :		
Qy	517 ACCCTGGCTATGCACCGCAATGCCATCAAACGTATGTACAGATCCAAACCTTCCTGGGC	576 : : : : :		
Db	102 --LeuGlnLeuGlnGlaAlaAspLeuSerAlaLeuArgLeuLeuGlaLeuGln	120 : : : :		
Qy	577 TCAGTCCCCAGCTACCTATCAGCTCTATGTGAGCCCTGATCTCTGCAGAGGTTCCCCTG	636 : : : : :		
Db	121 ThrGlyProHsiLeuLeuGlnThrTyrrValPheLeualaSerAspPheThrAspile	140 : : : : :		
Qy	637 GGTAGAGTTGTGCTAAATGGTATTTTCCCTGGTATCTGCACCTATGGGGCCACCCTTTC	696 : : : : :		
Db	141 ValproGlyValSerThrLeuPheSerTrpSerLeuSerTrpAlaLeu-	157 : : : : :		
Qy	697 AATATGTTGGCTATCCAGATCAAGTACGATCACTACAGATTCCGCTTGGGCCA--	750 : : : : :		
Db	158 -----ValSerTyrrArgPheMetGlyPheMetLysProGlyHis	171 : : : : :		
Qy	751 -----CTAGAAGTCTCTGCATCCACTCTGGCGSACATTTGGAGATCACT	795 : : : : :		
Db	172 LeualaMetProTrpalalaLeuPheCysGlnLeuLeuTrpArgMetGlyWeLeuGly	191 : : : : :		
Qy	796 TCCCGCTCTCTGATTTCTGTGTCTTCTCAGCCACTTTGAAAATTGAAGGCTGTGCCCTTC	855 : : : : :		
Db	192 ThrArgValleuSerLeuValleuPhe-----TyrLysAlaTyrrHisPhe	206 : : : : :		
Qy	856 CTAGTGTCAACTTCCTGATCATCTCTTTGAGCCTCGATT-----AAGTTCTGAGA	909 : : : : :		
Db	207 TrpVal-----PheValValaGlyAlaHisTrpLeuValMetThrPheTrpLeu	223 : : : : :		
Qy	910 AGTGGTGGCCAGATGCCCAATAACATTGAGAAAACTTTCAGC---CGSGTCGGCAGCTCTG	966 : : : : :		
Db	224 Val--AlaGlnGlnSerAspilelleasPserThrCysHisTrpArgLeuPheAsnLeu	242 : : : : :		
Qy	967 GTGTCCTGATTTTCAGTCACCACTCTATGTCGGCATCAACTCTCTTGTGTGTGACCT	1036 : : : : :		
Db	243 LeuValcylAlavalTyrrileuLeuCystyr-----LeuSerPheTrpAspSer	258 : : : : :		
Qy	1027 TTCGAGTTGAGGTTGGCAGACAGATCTCGTCGACAAAGGGCAGAACTGGGGACATATG	1086 : : : : :		
Db	259 -----ProSerArgAsnArgMet	264 : : : : :		
Qy	1087 GGCTGCACCTATAGTGTAGGTTGGTAGAATGTGATCATGCTCTGGTTTTTAAGTTC	1146 : : : : :		
Db	265 ValThrPheTyrrMetValMetLeuGlnAsnIlelLeuLeuLeuAlaThrAsp	284 : : : : :		
Qy	1147 TTT-----GGAGTGAAGGTGTTACTGTAATTAATCTGCTCAATCTCTGATTGCTTCAGCTC	1200 : : : : :		


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Db 285 PheLeuGlnGlyAla-----SerTrpThrSerLeuGlnThr 296
QY 1201 ATTATT-----GCTATCTGATTTCCATTGGCTTCATGCTCTTTCTTCAG 1248
Db 297 IleAlaGlyValLeuSerGlyPheLeuIleGlySerValSerLeuValIleTyrTrpSer 316
QY 1249 TACTTGCATCCA 1260
Db 317 LeuLeuHisPro 320

RESULT 11
US-10-176-758-524
; Sequence 524, Application US/10176758
; Publication No. US20030008353A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C104
; CURRENT APPLICATION NUMBER: US/10/176,758
; PRIORITY DATE: 2002-06-21
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 524
; LENGTH: 686
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-758-524

Alignment Scores:
Pred. No.: 0.000748 Length: 686
Score: 127.00 Matches: 81
Percent Similarity: 35.94% Conservative: 57
Best Local Similarity: 21.09% Mismatches: 158
Query Match: 4.99% Indels: 88
DB: 9 Gaps: 15

US-09-768-781-2 (1-1389) x US-10-176-758-524 (1-686)
QY 157 TCACCTTTTGTACTGTGGGAGGCTGCATCTGCTTTGTACATGGTTAGATCTATCGA 216
Db 9 SerAlaLeuLeuGlnAlaAlaGlnSerAlaArgLeuTyrThrValAlaTyrTrpPhe 28
QY 217 AAGAATAGTGAACCTACTGATGACATACACCTTTTCTTTCTTTATGTTTCATCATT 276
Db 29 ThrThrGlyArgLeuLeuTrpGlyTrpLeuAlaLeuAlaValLeuLeuProGlyPheLeu 48
QY 277 ATGGTCGAGTTGACCTTCATTTTGTGCACAGAGATCTAGCCAAAGATAAACCGCTATCA 336
Db 49 ValGlnAlaLeuSerTyrLeuTrpPheArgAlaAspGlyHisProGlyHisCysSerLeu 68
QY 337 TTATTTATGCATCTAATCTCTCTGGGACCTGTTATCATGATGTTTGGAGGCCATGATTAAG 396
Db 69 ValMetLeuHisLeuLeuGlnLeuGlyValTrpLysArgHisTrpAspAlaAlaLeuThr 88
QY 397 TACCTCACCTGTGGAGAAGAAGAGGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 456
Db 89 SerLeu-----GlnLysGlnLeuGlnAlaProHisArgGly----- 100
QY 457 AAGATGCTAATAGATGCGGAGGAGGTGCTGATAGTAAGTGGGAGGTGGGCCACTCCATCGG 516
Db 101 -----Trp----- 101
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QY 517 ACCGTGCTATGCACCGCAATGCTTACAAACGATATGTACAGATCCAAAGCCTTCTCGGC 576
Db 102 ---LeuGlnLeuGlnGlnAlaAspLeuSerAlaLeuArgLeuLeuGlnAlaLeuGln 120
QY 577 TCAGTGGCCCGAGCTGACCTATCAGCTCTATGTAGCCTGATCTCTGTGAGAGGTTCCTCG 636
Db 121 ThrGlyProHisLeuLeuGlnThrTyrValPheLeuAlaSerAspPheThrAspIle 140
QY 637 GGTAGAGTTGTGCTAATGTTATTTTCCCTGGTATCTGTACCTATGCGGCCACCTTTGC 696
Db 141 ValProGlyValSerThrLeuPheSerTrpSerSerLeuSerTrpAlaLeu----- 157
QY 697 AATATGTTGGCTATCCAGATCAAGTCAGTCACAAAGATTTCGCTTGGGCCA----- 750
Db 158 -----ValSerTyrThrArgPheMetGlyPheMetLysProGlyHis 171
QY 751 -----CTAGAAGTCTCTGCATCACCATCTCGCGGAGCATTTGGAGATCACT 795
Db 172 LeuAlaMetProTrpAlaAlaLeuPheCysGlnGlnLeuTrpArgMetGlyMetLeuGly 191
QY 796 TCCGCTCTCTGATTTCTGTGCTCTCTCTCAGCCACTTTGAAATTTGAAGCTGTGCCTTC 855
Db 192 ThrArgValLeuSerLeuValPhe-----TyrLysAlaTyrHisPhe 206
QY 856 CTAGTGTCAACTTCTCTGATCATCTCTTTGAGCCCTGGATT-----AAGTTCTGGAGA 909
Db 207 TrpVal-----PheValValAlaGlyAlaHisTrpLeuValMetThrPheTrpLeu 223
QY 910 AGTGTGCTCCAGATGCCCAATACATTGAGAAATACTTCAAC-----CGGTGCGCACTCTG 966
Db 224 Val---AlaGlnGlnSerAspIleIleAspSerThrCysHisTrpArgLeuPheAsnLeu 242
QY 967 GTGTCTCTGATTTCACTCAGTCACCATCTCTCTGCTGGCATCAACTCTCTGTGTCAGCT 1026
Db 243 LeuValGlyAlaValTyrIleLeuCysTyr-----LeuSerPheTrpAspSer 258
QY 1027 TTGCAGTTGAGGTTGGCAGACAGAGATCTCTCGCAAAAGGCGACACTGGGACATATG 1086
Db 259 -----ProserArgAsnArgMet 264
QY 1087 GGCCTGCATATAGTGTGAGGTTGGTAGAAGATGTGATCATGTCTTGGTTTAAAGTTC 1146
Db 265 ValThrPheTyrMetValMetLeuLeuGlnAlaAsnIleLeuLeuLeuAlaThrAsp 284
QY 1147 TTT-----GGAGTGAAGTGTACTGAATTAATGTCATTCCTTGAATTCCTTGCAGCTC 1200
Db 285 PheLeuGlnGlyAla-----SerTrpThrSerLeuGlnThr 296
QY 1201 ATTATT-----GCTATCTGATTTCCATTGGCTTCATGCTCTTTCTTCAG 1248
Db 297 IleAlaGlyValLeuSerGlyPheLeuIleGlySerValSerLeuValIleTyrTrpSer 316
QY 1249 TACTTGCATCCA 1260
Db 317 LeuLeuHisPro 320

RESULT 12
US-10-175-737-524
; Sequence 524, Application US/10175737
; Publication No. US200300013153A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
```

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; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C50
; CURRENT APPLICATION NUMBER: US/10/175,737
; CURRENT FILING DATE: 2002-06-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 524
; LENGTH: 686
; TYPE: ERT
; ORGANISM: Homo Sapien
US-10-175-737-524

Alignment Scores:
Pred. No.: 0.000748 Length: 686
Score: 127.00 Matches: 81
Percent Similarity: 35.94% Conservative: 57
Best Local Similarity: 21.09% Mismatches: 158
Query Match: 4.99% Indels: 88
DB: 9 Gaps: 15

US-09-768-781-2 (1-1389) x US-10-175-737-524 (1-686)
Qy 157 TCCACCTTTTGTACTGTGGGAGGCTGCATCTGCTTGTACATGTTAGATCTATCGA 216
Db 9 SerAlaLeuLeuGlnAlaAaGlnSerAlaAaGlyThrValAlaTyrPhe 28
Qy 217 AAGAAATAGTAACTTACTGTGATGATACATACCTTTTCTTTTATGTTTTCATCCATT 276
Db 29 ThrThrGlyArgLeuLeuTyrGlyTrpLeuAlaLeuAlaValLeuLeuProGlyPheLeu 48
Qy 277 ATGTGTCAGTTGACCTCATTTTGTTCACAGAGATCTAGCCAAAGATAAACCGGTATCA 336
Db 49 ValGlnAlaLeuSerTyrLeuTrpPheArgAlaAaGlyHisProGlyHisCysSerLeu 68
Qy 337 TTATTATGTCATTAATCTCTTGGGAGCTGTATCAGATGTTTGGAGCCCATGATTAAAG 396
Db 69 ValMetLeuHisLeuLeuGlnLeuGlyValTrpLysArgHisTrpAspAlaAlaLeuThr 88
Qy 397 TACCTCACACTGTGGAAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 456
Db 89 SerLeu-----GlnLysGlnLeuGlnAlaProHisArgGly----- 100
Qy 457 AAGATGCTAATAGATGGCGAGGAGGTGCTGATAGATGGGAGGTGGGCCACTCCATCCGG 516
Db 101 -----trp----- 101
Qy 517 ACCCTGGCTATGCACCGCAATGCCTACAAACGTATGTCACAGATCCAAAGCCTTCTCGGC 576
Db 102 ---LeuGlnLeuGlnGlnAlaAspLeuSerAlaLeuArgLeuLeuGlnAlaLeuGln 120
Qy 577 TCAGTGCCCGAGCTGACATCAGCTATGATGACCTGATCTGTGACAGAGGTTCCTCGT 636
Db 121 ThrGlyProHisLeuLeuGlnThrTrpValPheLeuAlaSerAspPheThrAspIle 140
Qy 637 GGTAGATTGTGCTAATGGTATTTTCCCTGGTATGTCACCTATGGGGCCACCTTTGC 696
Db 141 ValProGlyValSerThrLeuPheSerTrpSerLeuSerTrpAlaLeu----- 157
Qy 697 AATATGTTGGCTATCCAGATCAAGTACGATGATCAAGATTCGCTTGGGCCA----- 750
Db 158 -----ValSerTyrThrArgPheMetGlyPheMetLysProGlyHis 171
Qy 751 -----CTAGAAGTCTCTGTCATCACCATCTGGCGGACATTTGGAGATCACT 795
Db 172 LeuAlaMetProTrpAlaAlaLeuPheCysGlnGlnLeuTrpArgMetGlyMetLeuGly 191
Qy 796 TCCGCGCTCTGATTCCTGCTCTTCTTCTGAGCCACTTTTGAATTAAGAGCTGTGCTTC 855
Db 192 ThrArgValLeuSerLeuValLeuPhe-----TyrLysAlaTyrHisPhe 206
Qy 856 CTAGTGTCAACTCTCTGATCATCTCTTTGAGCCCTGGATT-----AAGTTCTGGAGA 909
Db ----- 909
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Db 207 TrpVal-----PheValValAlaGlyAlaHisTrpLeuValMetThrPheTrpLeu 223
Qy 910 AGTGTGTCAGATGCCAATAAATGAGAAAACTTCAGC---CGGTGCGGCACTCTG 966
Db 224 Val---AlaGlnGlnSerAspIleAspSerThrCysHisTrpArgLeuPheAsnLeu 242
Qy 967 GTGTCTCTGATTTTCACTCACCATCTCTATGCTGCGCATCAACTCTCTGCTGGTCAGCT 1026
Db 243 LeuValGlyAlaValTyrIleLeuCysTyr-----LeuSerPheTrpAspSer 258
Qy 1027 TTGCAGTTGAGGTTGGCAGACAGAGATCTCGTCGCAAAAGGCGCAACTGGGACATATG 1086
Db 259 -----ProSerArgAsnArgMet 264
Qy 1087 GGCCTGCATATAGTGTGAGGTTGTAGAGATGTGATCATGCTTGTGTTTAAAGTTC 1146
Db 265 ValThrPheTyrMetValMetLeuLeuGlnAsnIleLeuLeuLeuAlaThrAsp 284
Qy 1147 TTT-----GGAGTGAAAGTGTACTGAATTACTGCTGATTCCTGATTCCTGCTGAGCTC 1200
Db 285 PheLeuGlnGlyAla-----SerTrpThrSerLeuGlnThr 296
Qy 1201 ATTATT-----GCTTATCTGATTTCCATTTGCTGCTTCTCTTCTTCCAG 1248
Db 297 IleAlaGlyValLeuSerGlyPheLeuIleGlySerValSerLeuValIleTyrTyrSer 316
Qy 1249 TACTTGCATCCA 1260
Db 317 LeuLeuHisPro 320

RESULT 13
US-10-173-706-524
; Sequence 524, Application US/10173706
; Publication No. US20030022293A1
; GENERAL INFORMATION:
; APPLICANT: Baker Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C7
; CURRENT APPLICATION NUMBER: US/10/173,706
; CURRENT FILING DATE: 2002-06-17
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 524
; LENGTH: 686
; TYPE: ERT
; ORGANISM: Homo Sapien
US-10-173-706-524

Alignment Scores:
Pred. No.: 0.000748 Length: 686
Score: 127.00 Matches: 81
Percent Similarity: 35.94% Conservative: 57
Best Local Similarity: 21.09% Mismatches: 158
Query Match: 4.99% Indels: 88
DB: 9 Gaps: 15

US-09-768-781-2 (1-1389) x US-10-173-706-524 (1-686)
Qy 157 TCCACCTTTTGTACTGTGGGAGGCTGCATCTGCTTGTACATGTTAGATCTATCGA 216
Db 9 SerAlaLeuLeuGlnAlaAaGlnSerAlaAaGlyThrValAlaTyrPhe 28
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QY 217 AAGATAGTGAACTTACTGGATGACATACACCTTTCTTCTTTATGTTTTCATCATT 276
Db 29 ThrThrGlyArgLeuLeuTrpGlyTrpLeuAlaLeuValLeuLeuProGlyPheLeu 48
QY 277 ATGGTCACAGTTCACCTCTATTTTGTCCACAGAGATCTAGCAAGATAAACCCTATCA 336
Db 49 ValGlnAlaLeuSerTyxLeuTrpPheArgAlaAspGlyHisProGlyHisCysSerLeu 68
QY 337 TTATTTATCATCTAATCTCTTGGACCTGTTATCAGATGTTTGGAGGCCATGATTAAAG 396
Db 69 ValMetLeuHisLeuLeuGlnLeuGlyValTrpLysArgHisTrpAspAlaAlaLeuThr 88
QY 397 TACCTCACACTGTGGAAGAAGAGGAGGAGGAGCCCTATCTCAGCCTCACCCGAAAG 456
Db 89 SerLeu-----GlnLysGluLeuAlaProHisArgGly----- 100
QY 457 AAGATGCTAATAGATGCGGAGGAGGTGCTGATAGATGGGAGGTGGGCCACTCCATCCGG 516
Db 101 -----Trp----- 101
QY 517 ACCCTGGCTATGACCGCAATGCTTACAAACGTATGTACAGATCCAAAGCCTTCCTGGGC 576
Db 102 ---LeuGlnLeuGlnAlaAlaAspLeuSerAlaLeuArgLeuLeuGlnAlaLeuGln 120
QY 577 TCAGTGGCCCGACCTGACCTATCAGCTCTATGAGGCTGATCTCTCGAGAGGTTCCTCG 636
Db 121 ThrGlyProHisLeuLeuGlnThrValPheLeuAlaSerAspPheThrAspIle 140
QY 637 GGTAGAGTTGTCTAATGGTATTTTCCCTGGTATCTGTACCTATGGGCCACCTTTGC 696
Db 141 ValProGlyValSerThrLeuPheSerTrpSerLeuSerTrpAlaLeu----- 157
QY 697 AATATGTTGGCTATCCAGCAATCAAGTACAGTACTCAAGATTCGCCTTGGGCCA----- 750
Db 158 -----ValSerTyxThrArgPheMetGlyPheMetLysProGlyHis 171
QY 751 -----CTAGAAGTCTCTGCATCACCATCTGGCGGACATTTGGAGATCACT 795
Db 172 LeuAlaMetProTrpAlaAlaLeuPheCysGlnGlnLeuTrpArgMetGlyMetLeuGly 191
QY 796 TCCCGCTCTGATCTGTGTCTTCTCAGCCACTTTGAAATTGAAGCTGTGCCCTTC 855
Db 192 ThrArgValLeuSerLeuValLeuPhe-----TyrLysAlaTyxHisPhe 206
QY 856 CTAGTGCTCAACTTCTGTATCTCTTGTAGCCCTGGATT-----AAGTCTCTGGAGA 909
Db 207 TrpVal-----PheValValAlaGlyAlaHisTrpLeuValMetThrPheTrpLeu 223
QY 910 AGTGTGCCAGATGCCCAATTAACATTGAGAAAACCTCAGC---CGGTGGCAGCTCTG 966
Db 224 Val---AlaGlnGlnSerAspIleLeuAspSerThrCysHisTrpArgLeuPheAsnLeu 242
QY 967 GTGGTCTGATTTAGTCACTACCTCTATGCTGGCATCACTTCTTGTGCTGCTCAGCT 1026
Db 243 LeuValGlyAlaValTyxLeuLeuCysTyx-----LeuSerPheTrpAspSer 258
QY 1027 TTGCAGTTGAGGTGTGGCAGACAGATCTCTGTCGCAAAAGGGCAGAGTGGGGACATATG 1086
Db 259 -----ProSerArgAsnArgMet 264
QY 1087 GGCCTGCATATAGTGTGAGGTGTGAGAGATGTGATCATGCTCTGTGTTTAAAGTTC 1146
Db 265 ValThrPheTyxMetValMetLeuLeuGlnAlaAsnIleLeuLeuLeuAlaThrAsp 284
QY 1147 TTT-----GGAGTGAAGTGTACTGAATTACTGTCTTCTTGTGATTCCTTGCCTGAGCTC 1200
Db 285 PheLeuGlnGlyAla-----SerTrpThrSerLeuGlnThr 296
QY 1201 ATTATT-----GCTTATCTGATTTCCTATGCTTCCATGCTCTTCTTCTCCAG 1248
Db 297 IleAlaGlyValLeuSerGlyPheLeuIleGlySerValSerLeuValIleTyxSer 316
QY 1249 TACTTGCATCCA 1260

Db 317 LeuLeuHisPro 320
RESULT 14
; Sequence 524, Application US/10175738
; Publication No. US20030022294A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P34301C45
; CURRENT APPLICATION NUMBER: US/10/175,738
; CURRENT FILING DATE: 2002-06-19
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 524
; LENGTH: 686
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-175-738-524
Alignment Scores:
Pred. No.: 0.000748 Length: 686
Score: 127.00 Matches: 81
Percent Similarity: 35.94% Conservative: 57
Best Local Similarity: 21.09% Mismatches: 158
Query Match: 4.99% Indels: 88
DB: 9 Gaps: 15
US-09-768-781-2 (1-1389) x US-10-175-738-524 (1-686)
QY 157 TCACCTTTTGTACTGTGGGAGGTGCATCTGCTTTGTACATGTTAGTATCTATCGA 216
Db 9 SerAlaLeuLeuGlnAlaGlnSerAlaArgLeuTyxTrpValAlaTyxPhe 28
QY 217 AAGATAGTGAACTTACTGGATGACATACACCTTTCTTCTTTATGTTTTCATCATT 276
Db 29 ThrThrGlyArgLeuLeuTrpGlyTrpLeuAlaLeuValLeuLeuProGlyPheLeu 48
QY 277 ATGGTCACAGTTCACCTCTATTTTGTCCACAGAGATCTAGCAAGATAAACCCTATCA 336
Db 49 ValGlnAlaLeuSerTyxLeuTrpPheArgAlaAspGlyHisProGlyHisCysSerLeu 68
QY 337 TTATTTATCATCTAATCTCTTGGACCTGTTATCAGATGTTTGGAGGCCATGATTAAAG 396
Db 69 ValMetLeuHisLeuLeuGlnLeuGlyValTrpLysArgHisTrpAspAlaAlaLeuThr 88
QY 397 TACCTCACACTGTGGAAGAAGAGGAGGAGGAGCCCTATCTCAGCCTCACCCGAAAG 456
Db 89 SerLeu-----GlnLysGluLeuAlaProHisArgGly----- 100
QY 457 AAGATGCTAATAGATGCGGAGGAGGTGCTGATAGATGGGAGGTGGGCCACTCCATCCGG 516
Db 101 -----Trp----- 101
QY 517 ACCCTGGCTATGACCGCAATGCTTACAAACGTATGTACAGATCCAAAGCCTTCCTGGGC 576
Db 102 ---LeuGlnLeuGlnAlaAlaAspLeuSerAlaLeuArgLeuLeuGlnAlaLeuGln 120
QY 577 TCAGTGGCCCGACCTGACCTATCAGCTCTATGAGGCTGATCTCTCGAGAGGTTCCTCG 636
Db 121 ThrGlyProHisLeuLeuGlnThrValPheLeuAlaSerAspPheThrAspIle 140

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QY 637 GGTAGAGTTGTGCTAATGGTATTTTCCCTGGTATCTGTACACCTATGGGGCCACCTTTTGC 696
Db 141 ValProGlyValSerThrLeuPheSerTrpSerLeuSerLeuSerTrpAlaLeu----- 157
QY 697 AATATGTTGGCTATCCAGATCAAGTACAGTACACTACAAGATTCGCGCTTGGGCCA----- 750
Db 158 -----ValSerTyrThrArgPheMetGlyPheMetLysProGlyHis 171
QY 751 -----CTAGAAGTCTCTGTCATCACACTCTGGCGACATCTGGAGATCACT 795
Db 172 LeuAlaMetProTrpAlaLeuPheCysGlnGlnLeuTrpArgMetGlyMetLeuGly 191
QY 796 TCCGCGCTCTCGATTCTGGTCTCTTCTCAGCCACTTTGAAATTTGAAGGCTGTGCCCTTC 855
Db 192 ThrArgValLeuSerLeuValLeuPhe-----TyrLysAlaTyrHisPhe 206
QY 856 CTAGTGTCTCAACTTCTCTGATCATCTCTTTGAGCCCTGGATT-----AAGTTCTGGAGA 909
Db 207 TrpVal-----PheValValAlaGlyAlaHisTrpLeuValMetThrPheTrpLeu 223
QY 910 AGTGGTGGCCAGATGCCCAATAACATTGAGAAAAAATCTTCAGC---CGGGTCGGCACTCTG 966
Db 224 Val---AlaGlnGlnSerAspIleAspSerThrCysHisTrpArgLeuPheAsnLeu 242
QY 967 GTGTCCTGATTTCAGTCACCATCTCTATGCTGGCATCACTTCTTCTGCTGGTCAGCT 1026
Db 243 LeuValGlyAlaValTyrIleLeuCysTyr-----LeuSerPheTrpAspSer 258
QY 1027 TTGCAGTTTGAGTTGGCAGACAGAGATCTCGTCGACAAAGGCGCAACTGGGGACATATG 1086
Db 259 -----ProSerArgAsnArgMet 264
QY 1087 GGCTGTGCTACTAGTGTGAGTGTGGTAGAGATGTGATCGTCTGTGTTTAAAGTTC 1146
Db 265 ValThrPheTyrMetValMetLeuLeuGluAsnIleLeuLeuLeuAlaThrAsp 284
QY 1147 TTT-----GGAGTGAAGTGTACTGAATCTACTCTGATTCCTTCTGATTCGCTGAGCTC 1200
Db 285 PheLeuGlnGlyAla-----SerTrpThrSerLeuGlnThr 296
QY 1201 ATTATT-----GCTTATCTGATTTCCATTCTGCTTTCATGCTTCTCTTCTTCAG 1248
Db 297 IleAlaGlyValLeuSerGlyPheLeuIleGlySerValSerLeuValIleTyrTrpSer 316
QY 1249 TACTTGCATCCA 1260
Db 317 LeuLeuHisPro 320

RESULT 15
US-10-175-752-524
; Sequence 524, Application US/10175752
; Publication No. US20030022295A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Deenoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Par, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430RIC60
; CURRENT APPLICATION NUMBER: US/10/175,752
; CURRENT FILING DATE: 2002-06-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 524
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; LENGTH: 686
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-175-752-524

Alignment Scores:
Pred. No.: 0.000748 Length: 686
Score: 127.00 Matches: 81
Percent Similarity: 35.94% Conservative: 57
Best Local Similarity: 21.09% Mismatches: 158
Query Match: 4.99% Indels: 88
DB: 9 Gaps: 15

US-09-768-781-2 (1-1389) x US-10-175-752-524 (1-686)
QY 157 TCCACCTTTTGTACTGTGGGAGGCTGCATCTGCTTGTACATGGTTAGATCTATCA 216
Db 9 SerAlaLeuLeuGlnAlaAlaGlnSerAlaArgLeuTyrThrValAlaTyrTyrPhe 28
QY 217 AAGAATAGTGAACCTTACTGGATGACATACACCTTTTCTTTCTTTTATGTTTTCATCCATT 276
Db 29 ThrThrGlyArgLeuLeuTrpGlyTrpLeuAlaLeuAlaLeuLeuLeuProGlyPheLeu 48
QY 277 ATGTCTCCAGTTTGACCTCATTTTGTCCACAGAGATCTAGCCAAAGATAAACCGCTATCA 336
Db 49 ValGlnAlaLeuSerTyrLeuTrpPheArgAlaAspGlyHisProGlyHisCysSerLeu 68
QY 337 TTATTTATGCTATCAATCTCTTGGGACCTGTTATCAGATGTTTGGAGGCCATGATTAAAG 396
Db 69 ValMetLeuHisLeuLeuGlnLeuGlyValTrpLysArgHisTrpAspAlaAlaLeuThr 88
QY 397 TACCTCACACTGTGGAAGAAAGAGAGAGGAGGAGCCCTATGTGACGCTCACCCGAAAG 456
Db 89 SerLeu-----GlnLysGlnLeuGluAlaProHisArgGly----- 100
QY 457 AAGATGCTAATAGATGGCAGAGGTGCTGATAGAATGGAGGTGGGCCACTCCATCCGG 516
Db 101 -----Trp----- 101
QY 517 ACCCTGGCTATGACCGCAATGCCCTACAAAGTATGTACAGATCCAAAGCTTCTCTGGGC 576
Db 102 ---LeuGlnLeuGlnAlaAspLeuSerAlaLeuArgLeuLeuGluAlaLeuLeuGln 120
QY 577 TCAGTGGCCCCAGCTGACCTATCAGCTCTATGTGACCTGATCTCTGCAGAGGTTCCCTCG 636
Db 121 ThrGlyProHisLeuLeuLeuGlnThrTyrValPheLeuAlaSerAspPheThrAspIle 140
QY 637 GGTAGAGTTGTGCTAATGGTATTTTCCCTGGTATCTGTACCTATGGGCGGCCACCTTTGC 696
Db 141 ValProGlyValSerThrPhePheSerTrpSerLeuSerTrpAlaLeu----- 157
QY 697 AATATGTTGGCTATCCAGATCAAGTACAGTACACTACAAGATTCGCGCTTGGGCCA----- 750
Db 158 -----ValSerTyrThrArgPheMetGlyPheMetLysProGlyHis 171
QY 751 -----CTAGAAGTCTCTGTCATCACACTCTGGCGACATCTGGAGATCACT 795
Db 172 LeuAlaMetProTrpAlaLeuPheCysGlnGlnLeuTrpArgMetGlyMetLeuGly 191
QY 796 TCCGCGCTCTCGATTCTGGTCTCTTCTCAGCCACTTTTGAATTTGAAGGCTGTGCCCTTC 855
Db 192 ThrArgValLeuSerLeuValLeuPhe-----TyrLysAlaTyrHisPhe 206
QY 856 CTAGTGTCTCAACTTCTCTGATCATCTCTTTGAGCCCTGGATT-----AAGTTCTGGAGA 909
Db 207 TrpVal-----PheValValAlaGlyAlaHisTrpLeuValMetThrPheTrpLeu 223
QY 910 AGTGGTGGCCAGATGCCCAATAACATTGAGAAAAAATCTTCAGC---CGGGTCGGCACTCTG 966
Db 224 Val---AlaGlnGlnSerAspIleAspSerThrCysHisTrpArgLeuPheAsnLeu 242
QY 967 GTGTCCTGATTTCAGTCACCATCTCTATGCTGGCATCACTTCTTCTGCTGGTCAGCT 1026
Db 243 LeuValGlyAlaValTyrIleLeuCysTyr-----LeuSerPheTrpAspSer 258
QY 1027 TTGCAGTTTGAGTTGGCAGACAGAGATCTCGTCGACAAAGGCGCAACTGGGGACATATG 1086
Db 259 -----ProSerArgAsnArgMet 264
QY 1087 GGCTGTGCTACTAGTGTGAGTGTGGTAGAGATGTGATCGTCTGTGTTTAAAGTTC 1146
Db 265 ValThrPheTyrMetValMetLeuLeuGluAsnIleLeuLeuLeuAlaThrAsp 284
QY 1147 TTT-----GGAGTGAAGTGTACTGAATCTACTCTGATTCCTTCTGATTCGCTGAGCTC 1200
Db 285 PheLeuGlnGlyAla-----SerTrpThrSerLeuGlnThr 296
QY 1201 ATTATT-----GCTTATCTGATTTCCATTCTGCTTTCATGCTTCTCTTCTTCAG 1248
Db 297 IleAlaGlyValLeuSerGlyPheLeuIleGlySerValSerLeuValIleTyrTrpSer 316
QY 1249 TACTTGCATCCA 1260
Db 317 LeuLeuHisPro 320
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Db 243 LeuValGlyAlaValTyrIleLeuCysTyr-----LeuSerPheTyrAspSer 258
QY 1027 TTGCAGTTGAGTTGGCAGACAGAGATCTCGACAAAGGGCAGAACTGGGGACATATG 1086
Db 259 -----ProserArgAsnArgMet 264
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QY 1147 TTT-----GGAGTGAAGTGTACTGAATTACTGTCTATTCCTTGATTCCTGCAGCTC 1200
Db 285 PheLeuGlnGlyAla-----SerTyrThrSerLeuGlnThr 296
QY 1201 ATTATT-----GCTTATCTGATTTCCATTGGCTTCATGCTCCTTTCTTCCAG 1248
Db 297 IleAlaGlyValLeuSerGlyPheLeuIleGlySerValSerLeuValIleTyrTyrSer 316
QY 1249 TACTTGCATCCA 1260
Db 317 LeuLeuHisPro 320
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